SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Ashkenazi et al.

(ii) TITLE OF INVENTION: RTD Receptor

(iii) NUMBER OF SEQUENCES: 5

(iv) CORRESPONDENCE ADDRESS:
    (A) ADDRESSEE: Genentech, Inc.
    (B) STREET: 1 DNA Way
    (C) CITY: South San Francisco
    (D) STATE: California
    (E) COUNTRY: USA
    (F) ZIP: 94080

(v) COMPUTER READABLE FORM:
    (A) MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
    (B) COMPUTER: IBM PC compatible
    (C) OPERATING SYSTEM: PC-DOS/MS-DOS
    (D) SOFTWARE: WinPatin (Genentech)

(vi) CURRENT APPLICATION DATA:
    (A) APPLICATION NUMBER:
    (B) FILING DATE:
    (C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:
    (A) NAME: Marschang, Diane L.
    (B) REGISTRATION NUMBER: 35,600
    (C) REFERENCE/DOCKET NUMBER: P1129R1

(ix) TELECOMMUNICATION INFORMATION:
    (A) TELEPHONE: 650/225-5416
    (B) TELEFAX: 650/952-9881

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 386 amino acids
    (B) TYPE: Amino Acid
    (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Met Gly Leu Trp Gly Gln Ser Val Pro Thr Ala Ser Ser Ala Arg
1   5   10   15

Ala Gly Arg Tyr Pro Gly Ala Arg Thr Ala Ser Gly Thr Arg Pro
                20   25   30

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      Trp Leu Leu Asp Pro Lys Ile Leu Lys Phe Val Val Phe Ile Val
                      35              40                  45

      Ala Val Leu Leu Pro Val Arg Val Asp Ser Ala Thr Ile Pro Arg
  5                   50              55                  60

      Gln Asp Glu Val Pro Gln Gln Thr Val Ala Pro Gln Gln Gln Arg
                      65              70                  75

 10   Arg Ser Leu Lys Glu Glu Glu Cys Pro Ala Gly Ser His Arg Ser
                      80              85                  90

      Glu Tyr Thr Gly Ala Cys Asn Pro Cys Thr Glu Gly Val Asp Tyr
                      95             100                 105
 15
      Thr Ile Ala Ser Asn Asn Leu Pro Ser Cys Leu Leu Cys Thr Val
                     110             115                 120

      Cys Lys Ser Gly Gln Thr Asn Lys Ser Ser Cys Thr Thr Thr Arg
 20                  125             130                 135

      Asp Thr Val Cys Gln Cys Glu Lys Gly Ser Phe Gln Asp Lys Asn
                     140             145                 150

 25   Ser Pro Glu Met Cys Arg Thr Cys Arg Thr Gly Cys Pro Arg Gly
                     155             160                 165

      Met Val Lys Val Ser Asn Cys Thr Pro Arg Ser Asp Ile Lys Cys
                     170             175                 180

 30   Lys Asn Glu Ser Ala Ala Ser Ser Thr Gly Lys Thr Pro Ala Ala
                     185             190                 195

      Glu Glu Thr Val Thr Thr Ile Leu Gly Met Leu Ala Ser Pro Tyr
 35                  200             205                 210

      His Tyr Leu Ile Ile Ile Val Val Leu Val Ile Ile Leu Ala Val
                     215             220                 225

 40   Val Val Val Gly Phe Ser Cys Arg Lys Lys Phe Ile Ser Tyr Leu
                     230             235                 240

      Lys Gly Ile Cys Ser Gly Gly Gly Gly Gly Pro Glu Arg Val His
                     245             250                 255
 45
      Arg Val Leu Phe Arg Arg Arg Ser Cys Pro Ser Arg Val Pro Gly
                     260             265                 270

      Ala Glu Asp Asn Ala Arg Asn Glu Thr Leu Ser Asn Arg Tyr Leu
 50                  275             280                 285

      Gln Pro Thr Gln Val Ser Glu Gln Glu Ile Gln Gly Gln Glu Leu
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                  290                     295                     300
         Ala Glu Leu Thr Gly Val Thr Val Glu Xaa Pro Glu Glu Pro Gln
                         305                     310                     315
 5
         Arg Leu Leu Glu Gln Ala Glu Ala Glu Gly Cys Gln Arg Arg Arg
                         320                     325                     330

         Leu Leu Val Pro Val Asn Asp Ala Asp Ser Ala Asp Ile Ser Thr
10                       335                     340                     345

         Leu Leu Asp Ala Ser Ala Thr Leu Glu Glu Gly His Ala Lys Glu
                         350                     355                     360

15       Thr Ile Gln Asp Gln Leu Val Gly Ser Glu Lys Leu Phe Tyr Glu
                         365                     370                     375

         Glu Asp Glu Ala Gly Ser Ala Thr Ser Cys Leu
                         380                     385 386
```

20 (2) INFORMATION FOR SEQ ID NO:2:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 2082 base pairs
        (B) TYPE: Nucleic Acid
25   (C) STRANDEDNESS: Single
        (D) TOPOLOGY: Linear

   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

30

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CCAACTGCAC CTCGGTTCTA TCGATTGAAT TCCCCGGGGA TCCTCTAGAG 50

ATCCCTCGAC CTCGACCCAC GCGTCCGGAA CCTTTGCACG CGCACAAACT 100

ACGGGGACGA TTTCTGATTG ATTTTTGGCG CTTTCGATCC ACCCTCCTCC 150

CTTCTC  ATG GGA CTT TGG GGA CAA AGC GTC CCG ACC GCC 189
        Met Gly Leu Trp Gly Gln Ser Val Pro Thr Ala
         1               5                   10

TCG AGC GCT CGA GCA GGG CGC TAT CCA GGA GCC AGG ACA 228
Ser Ser Ala Arg Ala Gly Arg Tyr Pro Gly Ala Arg Thr
             15                  20

GCG TCG GGA ACC AGA CCA TGG CTC CTG GAC CCC AAG ATC 267
Ala Ser Gly Thr Arg Pro Trp Leu Leu Asp Pro Lys Ile
 25                  30                  35

CTT AAG TTC GTC GTC TTC ATC GTC GCG GTT CTG CTG CCG 306
Leu Lys Phe Val Val Phe Ile Val Ala Val Leu Leu Pro
         40                  45                  50
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         GTC CGG GTT GAC TCT GCC ACC ATC CCC CGG CAG GAC GAA 345
         Val Arg Val Asp Ser Ala Thr Ile Pro Arg Gln Asp Glu
                          55                  60

   5     GTT CCC CAG CAG ACA GTG GCC CCA CAG CAA CAG AGG CGC 384
         Val Pro Gln Gln Thr Val Ala Pro Gln Gln Gln Arg Arg
                  65                  70                  75

         AGC CTC AAG GAG GAG GAG TGT CCA GCA GGA TCT CAT AGA 423
  10     Ser Leu Lys Glu Glu Glu Cys Pro Ala Gly Ser His Arg
                      80                  85

         TCA GAA TAT ACT GGA GCC TGT AAC CCG TGC ACA GAG GGT 462
         Ser Glu Tyr Thr Gly Ala Cys Asn Pro Cys Thr Glu Gly
  15      90                  95                  100

         GTG GAT TAC ACC ATT GCT TCC AAC AAT TTG CCT TCT TGC 501
         Val Asp Tyr Thr Ile Ala Ser Asn Asn Leu Pro Ser Cys
                 105                 110                 115
  20
         CTG CTA TGT ACA GTT TGT AAA TCA GGT CAA ACA AAT AAA 540
         Leu Leu Cys Thr Val Cys Lys Ser Gly Gln Thr Asn Lys
                         120                 125

  25     AGT TCC TGT ACC ACG ACC AGA GAC ACC GTG TGT CAG TGT 579
         Ser Ser Cys Thr Thr Thr Arg Asp Thr Val Cys Gln Cys
                 130                 135                 140


         GAA AAA GGA AGC TTC CAG GAT AAA AAC TCC CCT GAG ATG 618
  30     Glu Lys Gly Ser Phe Gln Asp Lys Asn Ser Pro Glu Met
                         145                 150

         TGC CGG ACG TGT AGA ACA GGG TGT CCC AGA GGG ATG GTC 657
         Cys Arg Thr Cys Arg Thr Gly Cys Pro Arg Gly Met Val
  35     155                 160                 165

         AAG GTC AGT AAT TGT ACG CCC CGG AGT GAC ATC AAG TGC 696
         Lys Val Ser Asn Cys Thr Pro Arg Ser Asp Ile Lys Cys
                 170                 175                 180
  40
         AAA AAT GAA TCA GCT GCC AGT TCC ACT GGG AAA ACC CCA 735
         Lys Asn Glu Ser Ala Ala Ser Ser Thr Gly Lys Thr Pro
                         185                 190

  45     GCA GCG GAG GAG ACA GTG ACC ACC ATC CTG GGG ATG CTT 774
         Ala Ala Glu Glu Thr Val Thr Thr Ile Leu Gly Met Leu
                 195                 200                 205

         GCC TCT CCC TAT CAC TAC CTT ATC ATC ATA GTG GTT TTA 813
  50     Ala Ser Pro Tyr His Tyr Leu Ile Ile Ile Val Val Leu
                         210                 215
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     GTC ATC ATT TTA GCT GTG GTT GTG GTT GGC TTT TCA TGT 852
     Val Ile Ile Leu Ala Val Val Val Val Gly Phe Ser Cys
     220             225             230

  5  CGG AAG AAA TTC ATT TCT TAC CTC AAA GGC ATC TGC TCA 891
     Arg Lys Lys Phe Ile Ser Tyr Leu Lys Gly Ile Cys Ser
             235             240             245

     GGT GGT GGA GGA GGT CCC GAA CGT GTG CAC AGA GTC CTT 930
 10  Gly Gly Gly Gly Gly Pro Glu Arg Val His Arg Val Leu
                     250             255

     TTC CGG CGG CGT TCA TGT CCT TCA CGA GTT CCT GGG GCG 969
     Phe Arg Arg Arg Ser Cys Pro Ser Arg Val Pro Gly Ala
 15      260             265             270

     GAG GAC AAT GCC CGC AAC GAG ACC CTG AGT AAC AGA TAC 1008
     Glu Asp Asn Ala Arg Asn Glu Thr Leu Ser Asn Arg Tyr
                     275             280

 20  TTG CAG CCC ACC CAG GTC TCT GAG CAG GAA ATC CAA GGT 1047
     Leu Gln Pro Thr Gln Val Ser Glu Gln Glu Ile Gln Gly
     285             290             295

 25  CAG GAG CTG GCA GAG CTA ACA GGT GTG ACT GTA GAG TYG 1086
     Gln Glu Leu Ala Glu Leu Thr Gly Val Thr Val Glu Xaa
             300             305             310

     CCA GAG GAG CCA CAG CGT CTG CTG GAA CAG GCA GAA GCT 1125
 30  Pro Glu Glu Pro Gln Arg Leu Leu Glu Gln Ala Glu Ala
                     315             320

     GAA GGG TGT CAG AGG AGG AGG CTG CTG GTT CCA GTG AAT 1164
     Glu Gly Cys Gln Arg Arg Arg Leu Leu Val Pro Val Asn
 35      325             330             335

     GAC GCT GAC TCC GCT GAC ATC AGC ACC TTG CTG GAT GCC 1203
     Asp Ala Asp Ser Ala Asp Ile Ser Thr Leu Leu Asp Ala
                     340             345

 40  TCG GCA ACA CTG GAA GAA GGA CAT GCA AAG GAA ACA ATT 1242
     Ser Ala Thr Leu Glu Glu Gly His Ala Lys Glu Thr Ile
     350             355             360

 45  CAG GAC CAA CTG GTG GGC TCC GAA AAG CTC TTT TAT GAA 1281
     Gln Asp Gln Leu Val Gly Ser Glu Lys Leu Phe Tyr Glu
             365             370             375

     GAA GAT GAG GCA GGC TCT GCT ACG TCC TGC CTG TGAAAG 1320
 50  Glu Asp Glu Ala Gly Ser Ala Thr Ser Cys Leu
                     380             385 386
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AATCTCTTCA GGAAACCAGA GCTTCCCTCA TTTACCTTTT CTCCTACAAA 1370

GGGAAGCAGC CTGGAAGAAA CAGTCCAGTA CTTGACCCAT GCCCCAACAA 1420

ACTCTACTAT CCAATATGGG GCAGCTTACC AATGGTCCTA GAACTTTGTT 1470

AACGCACTTG GAGTAATTTT TATGAAATAC TGCGTGTGAT AAGCAAACGG 1520

GAGAAATTTA TATCAGATTC TTGGCTGCAT AGTTATACGA TTGTGTATTA 1570

AGGGTCGTTT TAGGCCACAT GCGGTGGCTC ATGCCTGTAA TCCCAGCACT 1620

TTGATAGGCT GAGGCAGGTG GATTGCTTGA GCTCGGGAGT TTGAGACCAG 1670

CCTCATCAAC ACAGTGAAAC TCCATCTCAA TTTAAAAGA AAAAAGTGG 1720

TTTTAGGATG TCATTCTTTG CAGTTCTTCA TCATGAGACA AGTCTTTTTT 1770

TCTGCTTCTT ATATTGCAAG CTCCATCTCT ACTGGTGTGT GCATTTAATG 1820

ACATCTAACT ACAGATGCCG CACAGCCACA ATGCTTTGCC TTATAGTTTT 1870

TTAACTTTAG AACGGGATTA TCTTGTTATT ACCTGTATTT TCAGTTTCGG 1920

ATATTTTTGA CTTAATGATG AGATTATCAA GACGTACCCC TATGCTAAGT 1970

CATGAGCATA TGGACTTACG AGGGTTCGAC TTAGAGTTTT GAGCTTTAAG 2020

ATAGGATTAT TGGGGGCTTA CCCCCACCTT AATTAGAAGA AACATTTTAT 2070

ATTGCTTTAC TA 2082

(2) INFORMATION FOR SEQ ID NO:3:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 50 base pairs
        (B) TYPE: Nucleic Acid
        (C) STRANDEDNESS: Single
        (D) TOPOLOGY: Linear

   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CATAAAAGTT CCTGCACCAT GACCAGAGAC ACAGTGTGTC AGTGTAAAGA 50

(2) INFORMATION FOR SEQ ID NO:4:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 24 base pairs
        (B) TYPE: Nucleic Acid
        (C) STRANDEDNESS: Single
        (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CTTCAGGAAA CCAGAGCTTC CCTC 24

5

(2) INFORMATION FOR SEQ ID NO:5:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 24 base pairs

10
        (B) TYPE: Nucleic Acid
        (C) STRANDEDNESS: Single
        (D) TOPOLOGY: Linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

15

TTCTCCCGTT TGCTTATCAC ACGC 24